FIG. 1

<400> 5
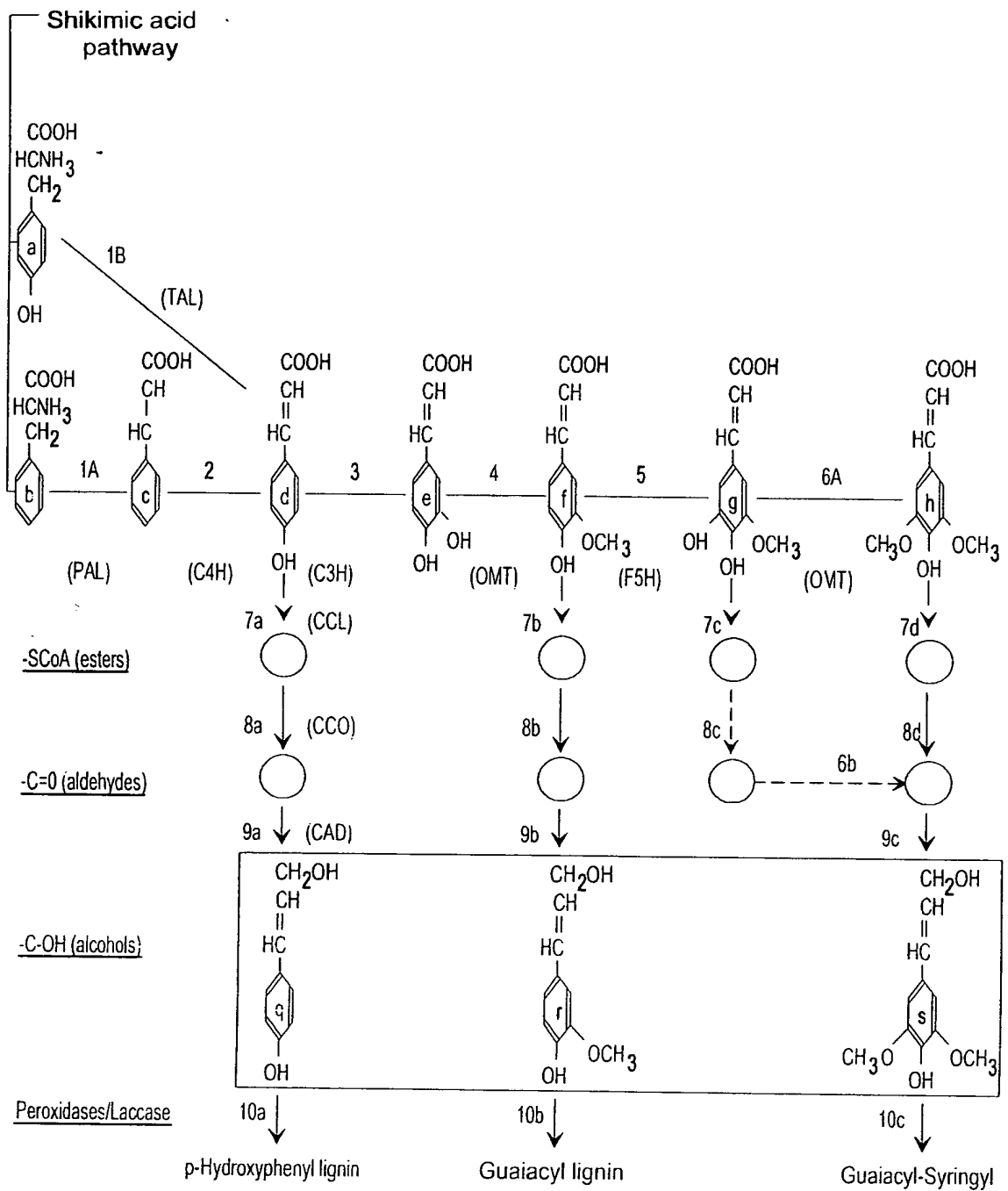
cggcacgagc cctacctcct ttcttggaaa aatttcccca ttcgatcaca atccgggcct 60

caaaaa atg gga tca aca agc gaa acg aag atg agc ccg agt gaa gca	108
Met Gly Ser Thr Ser Glu Thr Lys Met Ser Pro Ser Glu Ala	
1 5 10	

gca gca gca gaa gaa gaa gca ttc gta ttc gct atg caa tta acc agt	156
Ala Ala Ala Glu Glu Glu Ala Phe Val Phe Ala Met Gln Leu Thr Ser	
15 20 25 30	

gct tca gtt ctt ccc atg gtc cta aaa tca gcc ata gag ctc gac gtc	204
Ala Ser Val Leu Pro Met Val Leu Lys Ser Ala Ile Glu Leu Asp Val	
35 40 45	

tta gaa atc atg gct aaa gct ggt cca ggt gcg cac ata tcc aca tct	252
Leu Glu Ile Met Ala Lys Ala Gly Pro Gly Ala His Ile Ser Thr Ser	
50 55 60	

gac ata gcc tct aag ctg ccc aca aag aat cca gat gca gcc gtc atg	300
Asp Ile Ala Ser Lys Leu Pro Thr Lys Asn Pro Asp Ala Ala Val Met	
65 70 75	

ctt gac cgt atg ctc cgc ctc ttg gct agc tac tct gtt cta acg tgc	348
Leu Asp Arg Met Leu Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys	
80 85 90	

tct ctc cgc acc ctc cct gac ggc aag atc gag agg ctt tac ggc ctt	396
Ser Leu Arg Thr Leu Pro Asp Gly Lys Ile Glu Arg Leu Tyr Gly Leu	
95 100 105 110	

gca ccc gtt tgt aaa ttc ttg acc aga aac gat gat gga gtc tcc ata	444
Ala Pro Val Cys Lys Phe Leu Thr Arg Asn Asp Asp Gly Val Ser Ile	
115 120 125	

gcc gct ctg tct ctc atg aat caa gac aag gtc ctc atg gag agc tgg	492
Ala Ala Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp	
130 135 140	

tac cac ttg acc gag gca gtt ctt gaa ggt gga att cca ttt aac aag	540
Tyr His Leu Thr Glu Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys	
145 150 155	

Fig. 2A

```
gcc tat gga atg aca gca ttt gag tac cat ggc acc gat ccc aga ttc    588
Ala Tyr Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe
    160             165             170

aac aca gtt ttc aac aat gga atg tcc aat cat tcg acc att acc atg    636
Asn Thr Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met
175             180             185             190

aag aaa atc ctt gag act tac aaa ggg ttc gag gga ctt gga tct gtg    684
Lys Lys Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val
                195             200             205

gtt gat gtt ggt ggt ggc act ggt gcc cac ctt aac atg att atc gct    732
Val Asp Val Gly Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala
            210             215             220

aaa tac ccc atg atc aag ggc att aac ttc gac ttg cct cat gtt att    780
Lys Tyr Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile
            225             230             235

gag gag gct ccc tcc tat cct ggt gtg gag cat gtt ggt gga gat atg    828
Glu Glu Ala Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met
    240             245             250

ttt gtt agt gtt cca aaa gga gat gcc att ttc atg aag tgg ata tgt    876
Phe Val Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys
255             260             265             270

cat gat tgg agc gat gaa cac tgc ttg aag ttt ttg aag aaa tgt tat    924
His Asp Trp Ser Asp Glu His Cys Leu Lys Phe Leu Lys Lys Cys Tyr
                275             280             285

gaa gca ctt cca acc aat ggg aag gtg atc ctt gct gaa tgc atc ctc    972
Glu Ala Leu Pro Thr Asn Gly Lys Val Ile Leu Ala Glu Cys Ile Leu
            290             295             300

ccc gtg gcg cca gac gca agc ctc ccc act aag gca gtg gtc cat att   1020
Pro Val Ala Pro Asp Ala Ser Leu Pro Thr Lys Ala Val Val His Ile
            305             310             315

gat gtc atc atg ttg gct cat aac cca ggt ggg aaa gag aga act gag   1068
Asp Val Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu
    320             325             330

aag gag ttt gag gcc ttg gcc aag ggg gct gga ttt gaa ggt ttc cga   1116
Lys Glu Phe Glu Ala Leu Ala Lys Gly Ala Gly Phe Glu Gly Phe Arg
```

Fig. 2B

```
335                  340                 345                  350

gta gta gcc tcg tgc gct tac aat aca tgg atc atc gaa ttt ttg aag      1164
Val Val Ala Ser Cys Ala Tyr Asn Thr Trp Ile Ile Glu Phe Leu Lys
                355                 360                  365

aag att tgagtcctta ctcggctttg agtacataat accaactcct tttggttttc      1220
Lys Ile

gagattgtga ttgtgattgt gattgtctct ctttcgcagt tggccttatg atataatgta  1280

tcgttaactc gatcacagaa gtgcaaaaga cagtgaatgt acactgcttt ataaaataaa  1340

aattttaaga ttttgattca tgtaaaaaaa aaaaaaaaaa                        1380
```

Fig. 2C

SEQ ID 6

<400> 6

Met 1	Gly	Ser	Thr	Ser 5	Glu	Thr	Lys	Met	Ser 10	Pro	Ser	Glu	Ala	Ala 15	Ala

Met Gly Ser Thr Ser Glu Thr Lys Met Ser Pro Ser Glu Ala Ala Ala
 1   5   10   15

Ala Glu Glu Glu Ala Phe Val Phe Ala Met Gln Leu Thr Ser Ala Ser
            20   25   30

Val Leu Pro Met Val Leu Lys Ser Ala Ile Glu Leu Asp Val Leu Glu
            35   40   45

Ile Met Ala Lys Ala Gly Pro Gly Ala His Ile Ser Thr Ser Asp Ile
        50   55   60

Ala Ser Lys Leu Pro Thr Lys Asn Pro Asp Ala Ala Val Met Leu Asp
65   70   75   80

Arg Met Leu Arg Leu Leu Ala Ser Tyr Ser Val Leu Thr Cys Ser Leu
                85   90   95

Arg Thr Leu Pro Asp Gly Lys Ile Glu Arg Leu Tyr Gly Leu Ala Pro
            100   105   110

Val Cys Lys Phe Leu Thr Arg Asn Asp Asp Gly Val Ser Ile Ala Ala
        115   120   125

Leu Ser Leu Met Asn Gln Asp Lys Val Leu Met Glu Ser Trp Tyr His
    130   135   140

Leu Thr Glu Ala Val Leu Glu Gly Gly Ile Pro Phe Asn Lys Ala Tyr
145   150   155   160

Gly Met Thr Ala Phe Glu Tyr His Gly Thr Asp Pro Arg Phe Asn Thr
            165   170   175

Val Phe Asn Asn Gly Met Ser Asn His Ser Thr Ile Thr Met Lys Lys
            180   185   190

Ile Leu Glu Thr Tyr Lys Gly Phe Glu Gly Leu Gly Ser Val Val Asp
        195   200   205

Val Gly Gly Gly Thr Gly Ala His Leu Asn Met Ile Ile Ala Lys Tyr
        210   215   220

Pro Met Ile Lys Gly Ile Asn Phe Asp Leu Pro His Val Ile Glu Glu
225   230   235   240

Fig. 2D

SEQ ID 6

```
Ala Pro Ser Tyr Pro Gly Val Glu His Val Gly Gly Asp Met Phe Val
            245             250             255

Ser Val Pro Lys Gly Asp Ala Ile Phe Met Lys Trp Ile Cys His Asp
            260             265             270

Trp Ser Asp Glu His Cys Leu Lys Phe Leu Lys Lys Cys Tyr Glu Ala
            275             280             285

Leu Pro Thr Asn Gly Lys Val Ile Leu Ala Glu Cys Ile Leu Pro Val
    290             295             300

Ala Pro Asp Ala Ser Leu Pro Thr Lys Ala Val Val His Ile Asp Val
305             310             315             320

Ile Met Leu Ala His Asn Pro Gly Gly Lys Glu Arg Thr Glu Lys Glu
            325             330             335

Phe Glu Ala Leu Ala Lys Gly Ala Gly Phe Glu Gly Phe Arg Val Val
            340             345             350

Ala Ser Cys Ala Tyr Asn Thr Trp Ile Ile Glu Phe Leu Lys Lys Ile
            355             360             365
```

Fig. 2E

SEQ ID 7

<400> 7

```
cggcacgagc tcattttcca cttctggttt gatctctgca attcttccat cagtcccta    59
```

```
atg gag acc caa aca aaa caa gaa gaa atc ata tat cgg tcg aaa ctc    107
Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
 1               5                   10                  15
```

```
ccc gat atc tac atc ccc aaa cac ctc cct tta cat tcg tat tgt ttc    155
Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
                20                  25                  30
```

```
gag aac atc tca cag ttc ggc tcc cgc ccc tgt ctg atc aat ggc gca    203
Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
            35                  40                  45
```

```
acg ggc aag tat tac aca tat gct gag gtt gag ctc att gcg cgc aag    251
Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys
        50                  55                  60
```

```
gtc gca tcc ggc ctc aac aaa ctc ggc gtt cga caa ggt gac atc atc    299
Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
65                  70                  75                  80
```

```
atg ctt ttg cta ccc aac tcg ccg gag ttc gtg ttt tca att ctc ggc    347
Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
                85                  90                  95
```

```
gca tcc tac cgc ggg gct gcc gcc acc gcc gca aac ccg ttt tat acc    395
Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr
                100                 105                 110
```

```
cct gcc gag atc agg aag caa gcc aaa acc tcc aac gcc agg ctt att    443
Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile
            115                 120                 125
```

```
atc aca cat gcc tgt tac tat gag aaa gtg aag gac ttg gtg gaa gag    491
Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu
        130                 135                 140
```

```
aac gtt gcc aag atc ata tgt ata gac tca ccc ccg gac ggt tgt ttg    539
Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu
145                 150                 155                 160
```

Fig. 3A

```
cac ttc tcg g.,g ctg agt gag gcg gac gag aac gac atg ccc aat gta    587
His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val
                165             170             175

gag att gac ccc gat gat gtg gtg gcg ctg ccg tac tcg tca ggg acg    635
Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr
            180             185             190

acg ggt tta cca aag ggg gtg atg cta aca cac aag gga caa gtg acg    683
Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr
        195             200             205

agt gtg gcg caa cag gtg gac gga gag aat ccg aac ctg tat ata cat    731
Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His
    210             215             220

agc gag gac gtg gtt ctg tgc gtg ttg cct ctg ttt cac atc tac tcg    779
Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser
225             230             235             240

atg aac gtc atg ttt tgc ggg tta cga gtt ggt gcg gcg att ctg att    827
Met Asn Val Met Phe Cys Gly Leu Arg Val Gly Ala Ala Ile Leu Ile
                245             250             255

atg cag aaa ttt gaa ata tat ggg ttg tta gag ctg gtc aga agt aca    875
Met Gln Lys Phe Glu Ile Tyr Gly Leu Leu Glu Leu Val Arg Ser Thr
            260             265             270

ggt gac cat cat gcc tat cgt aca ccc atc gta ttg gca atc tcc aag    923
Gly Asp His His Ala Tyr Arg Thr Pro Ile Val Leu Ala Ile Ser Lys
        275             280             285

act ccg gat ctt cac aac tat gat gtg tcc tcc att cgg act gtc atg    971
Thr Pro Asp Leu His Asn Tyr Asp Val Ser Ser Ile Arg Thr Val Met
        290             295             300

tca ggt gcg gct cct ctg ggc aag gaa ctt gaa gat tct gtc aga gct    1019
Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ser Val Arg Ala
305             310             315             320

aag ttt ccc acc gcc aaa ctt ggt cag gga tat gga atg acg gag gca    1067
Lys Phe Pro Thr Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala
            325             330             335

ggg ccc gtg cta gcg atg tgt ttg gca ttt gcc aag gaa ggg ttt gaa    1115
Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Gly Phe Glu
            340             345             350
```

Fig. 3B

```
ata aaa tcg ggg gca tct gga act gtt tta agg aac gca cag atg aag    1163
Ile Lys Ser Gly Ala Ser Gly Thr Val Leu Arg Asn Ala Gln Met Lys
        355             360              365

att gtg gac cct gaa acc ggt gtc act ctc cct cga aac caa ccc gga    1211
Ile Val Asp Pro Glu Thr Gly Val Thr Leu Pro Arg Asn Gln Pro Gly
        370             375              380

gag att tgc att aga gga gac caa atc atg aaa ggt tat ctt aat gat    1259
Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp
385             390              395              400

cct gag gcg acg gag aga acc ata gac aag gaa ggt tgg tta cac aca    1307
Pro Glu Ala Thr Glu Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr
            405             410              415

ggt gat gtg ggc tac atc gac gat gac act gag ctc ttc att gtt gat    1355
Gly Asp Val Gly Tyr Ile Asp Asp Asp Thr Glu Leu Phe Ile Val Asp
            420             425              430

cgg ttg aag gaa ctg atc aaa tac aaa ggg ttt cag gtg gca ccc gct    1403
Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala
        435             440              445

gag ctt gag gcc atg ctc ctc aac cat ccc aac atc tct gat gct gcc    1451
Glu Leu Glu Ala Met Leu Leu Asn His Pro Asn Ile Ser Asp Ala Ala
        450             455              460

gtc gtc cca atg aaa gac gat gaa gct gga gag ctc cct gtg gcg ttt    1499
Val Val Pro Met Lys Asp Asp Glu Ala Gly Glu Leu Pro Val Ala Phe
465             470              475              480

gtt gta aga tca gat ggt tct cag ata tcc gag gct gaa atc agg caa    1547
Val Val Arg Ser Asp Gly Ser Gln Ile Ser Glu Ala Glu Ile Arg Gln
            485             490              495

tac atc gca aaa cag gtg gtt ttt tat aaa aga ata cat cgc gta ttt    1595
Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Ile His Arg Val Phe
            500             505              510

ttc gtc gaa gcc att cct aaa gcg ccc tct ggc aaa atc ttg cgg aag    1643
Phe Val Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys Ile Leu Arg Lys
            515             520              525

gac ctg aga gcc aaa ttg gcg tct ggt ctt ccc aat taattctcat        1689
Asp Leu Arg Ala Lys Leu Ala Ser Gly Leu Pro Asn
        530             535              540
```

Fig. 3C

```
tcgctaccct cctttctctt atcatacgcc aacacgaacg aagaggctca attaaacgct 1749

gctcattcga agcggctcaa ttaaagctgc tcattcatgt ccaccgagtg ggcagcctgt 1809

cttgttggga tgttctttca tttgattcag ctgtgagaag ccagaccctc attatttatt 1869

gtgaaattca caagaatgtc tgtaaatcga tgttgtgagt gatgggtttc aaaacacttt 1929

tgacattgtt tacgttgtat ttcctgctgt tgaaaataac tactttgtat gacttttatt 1989

tgggaagata acctttcaaa aaaaaaaaaa aaaaaa                       2025
```

Fig. 3D

SEQ ID 8

```
Met Glu Thr Gln Thr Lys Gln Glu Glu Ile Ile Tyr Arg Ser Lys Leu
 1               5               10                  15

Pro Asp Ile Tyr Ile Pro Lys His Leu Pro Leu His Ser Tyr Cys Phe
            20              25                  30

Glu Asn Ile Ser Gln Phe Gly Ser Arg Pro Cys Leu Ile Asn Gly Ala
          35                  40                  45

Thr Gly Lys Tyr Tyr Thr Tyr Ala Glu Val Glu Leu Ile Ala Arg Lys
        50              55                  60

Val Ala Ser Gly Leu Asn Lys Leu Gly Val Arg Gln Gly Asp Ile Ile
 65              70                  75                  80

Met Leu Leu Leu Pro Asn Ser Pro Glu Phe Val Phe Ser Ile Leu Gly
                85                  90                  95

Ala Ser Tyr Arg Gly Ala Ala Ala Thr Ala Ala Asn Pro Phe Tyr Thr
            100             105                 110

Pro Ala Glu Ile Arg Lys Gln Ala Lys Thr Ser Asn Ala Arg Leu Ile
        115             120                 125

Ile Thr His Ala Cys Tyr Tyr Glu Lys Val Lys Asp Leu Val Glu Glu
    130             135                 140

Asn Val Ala Lys Ile Ile Cys Ile Asp Ser Pro Pro Asp Gly Cys Leu
145             150                 155                 160

His Phe Ser Glu Leu Ser Glu Ala Asp Glu Asn Asp Met Pro Asn Val
                165                 170                 175

Glu Ile Asp Pro Asp Asp Val Val Ala Leu Pro Tyr Ser Ser Gly Thr
            180                 185                 190

Thr Gly Leu Pro Lys Gly Val Met Leu Thr His Lys Gly Gln Val Thr
        195                 200                 205

Ser Val Ala Gln Gln Val Asp Gly Glu Asn Pro Asn Leu Tyr Ile His
    210                 215                 220

Ser Glu Asp Val Val Leu Cys Val Leu Pro Leu Phe His Ile Tyr Ser
225                 230                 235                 240
```

Fig. 3E

Met Asn Val Met Phe Cys Gly Leu Arg Val Gly Ala Ala Ile Leu Ile
            245   250   255

Met Gln Lys Phe Glu Ile Tyr Gly Leu Leu Glu Leu Val Arg Ser Thr
            260   265   270

Gly Asp His His Ala Tyr Arg Thr Pro Ile Val Leu Ala Ile Ser Lys
        275   280   285

Thr Pro Asp Leu His Asn Tyr Asp Val Ser Ser Ile Arg Thr Val Met
    290   295   300

Ser Gly Ala Ala Pro Leu Gly Lys Glu Leu Glu Asp Ser Val Arg Ala
305   310   315   320

Lys Phe Pro Thr Ala Lys Leu Gly Gln Gly Tyr Gly Met Thr Glu Ala
            325   330   335

Gly Pro Val Leu Ala Met Cys Leu Ala Phe Ala Lys Glu Gly Phe Glu
            340   345   350

Ile Lys Ser Gly Ala Ser Gly Thr Val Leu Arg Asn Ala Gln Met Lys
        355   360   365

Ile Val Asp Pro Glu Thr Gly Val Thr Leu Pro Arg Asn Gln Pro Gly
    370   375   380

Glu Ile Cys Ile Arg Gly Asp Gln Ile Met Lys Gly Tyr Leu Asn Asp
385   390   395   400

Pro Glu Ala Thr Glu Arg Thr Ile Asp Lys Glu Gly Trp Leu His Thr
            405   410   415

Gly Asp Val Gly Tyr Ile Asp Asp Asp Thr Glu Leu Phe Ile Val Asp
            420   425   430

Arg Leu Lys Glu Leu Ile Lys Tyr Lys Gly Phe Gln Val Ala Pro Ala
        435   440   445

Glu Leu Glu Ala Met Leu Leu Asn His Pro Asn Ile Ser Asp Ala Ala
    450   455   460

Val Val Pro Met Lys Asp Asp Glu Ala Gly Glu Leu Pro Val Ala Phe
465   470   475   480

SEQ ID 8

```
Val Val Arg Ser Asp Gly Ser Gln Ile Ser Glu Ala Glu Ile Arg Gln
            485             490             495

Tyr Ile Ala Lys Gln Val Val Phe Tyr Lys Arg Ile His Arg Val Phe
            500             505             510

Phe Val Glu Ala Ile Pro Lys Ala Pro Ser Gly Lys Ile Leu Arg Lys
            515             520             525

Asp Leu Arg Ala Lys Leu Ala Ser Gly Leu Pro Asn
    530             535             540
```

Fig. 3G

```
cggcacgagg aaaccctaaa actcacctct cttacccttt ctcttca atg gct ttc      56
                                                        Met Ala Phe
                                                          1

ctt cta ata ccc atc tca ata atc ttc atc gtc tta gct tac cag ctc      104
Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala Tyr Gln Leu
        5              10              15

tat caa cgg ctc aga ttt aag ctc cca ccc ggc cca cgt cca tgg ccg      152
Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg Pro Trp Pro
 20              25              30              35

atc gtc gga aac ctt tac gac ata aaa ccg gtg agg ttc cgg tgt ttc      200
Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe Arg Cys Phe
             40              45              50

gcc gag tgg tca caa gcg tac ggt ccg atc ata tcg gtg tgg ttc ggt      248
Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val Trp Phe Gly

            55              60              65

tca acg ttg aat gtg atc gta tcg aat tcg gaa ttg gct aag gaa gtg      296
Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala Lys Glu Val
            70              75              80

ctc aag gaa aaa gat caa caa ttg gct gat agg cat agg agt aga tca      344
Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg Ser Arg Ser
        85              90              95

gct gcc aaa ttt agc agg gat ggg cag gac ctt ata tgg gct gat tat      392
Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp Ala Asp Tyr
100             105             110             115

gga cct cac tat gtg aag gtt aca aag gtt tgt acc ctc gag ctt ttt      440
Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu Glu Leu Phe
            120             125             130

act cca aag cgg ctt gaa gct ctt aga ccc att aga gaa gat gaa gtt      488
Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu Asp Glu Val
            135             140             145

aca gcc atg gtt gag tcc att ttt aat gac act gcg aat cct gaa aat      536
Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn Pro Glu Asn
            150             155             160
```

Fig. 4A

```
tat ggg aag agt atg ctg gtg aag aag tat ttg gga gca gta gca ttc   584
Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala Val Ala Phe
    165                 170                 175

aac aac att aca aga ctc gca ttt gga aag cga ttc gtg aat tca gag   632
Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val Asn Ser Glu
180                 185                 190                 195

ggt gta atg gac gag caa gga ctt gaa ttt aag gaa att gtg gcc aat   680
Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile Val Ala Asn
                200                 205                 210

gga ctc aag ctt ggt gcc tca ctt gca atg gct gag cac att cct tgg   728
Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His Ile Pro Trp
            215                 220                 225

ctc cgt tgg atg ttc cca ctt gag gaa ggg gcc ttt gcc aag cat ggg   776
Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala Lys His Gly
            230                 235                 240

gca cgt agg gac cga ctt acc aga gct atc atg gaa gag cac aca ata   824
Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu His Thr Ile
    245                 250                 255

gcc cgt aaa aag agt ggt gga gcc caa caa cat ttc gtg gat gca ttg   872
Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val Asp Ala Leu
260                 265                 270                 275

ctc acc cta caa gag aaa tat gac ctt agc gag gac act att att ggg   920
Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr Ile Ile Gly
                280                 285                 290

ctc ctt tgg gat atg atc act gca ggc atg gac aca acc gca atc tct   968
Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr Ala Ile Ser
            295                 300                 305

gtc gaa tgg gcc atg gcc gag tta att aag aac cca agg gtg caa caa  1016
Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg Val Gln Gln
            310                 315                 320

aaa gct caa gag gag cta gac aat gta ctt ggg tcc gaa cgt gtc ctg  1064
Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu Arg Val Leu
    325                 330                 335
```

Fig. 4B

```
acc gaa ttg gac ttc tca agc ctc cct tat cta caa tgt gta gcc aag       1112
Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys Val Ala Lys
340                 345                 350                 355


gag gca cta agg ctg cac cct cca aca cca cta atg ctc cct cat cgc       1160
Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu Pro His Arg
                360                 365                 370


gcc aat gcc aac gtc aaa att ggt ggc tac gac atc cct aag gga tca       1208
Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro Lys Gly Ser
            375                 380                 385


aat gtt cat gta aat gtc tgg gcc gtg gct cgt gat cca gca gtg tgg       1256
Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro Ala Val Trp
            390                 395                 400


cgt gac cca cta gag ttt cga ccg gaa cgg ttc tct gaa gac gat gtc       1304
Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu Asp Asp Val
        405                 410                 415


gac atg aaa ggt cac gat tat agg cta ctg ccg ttt ggt gca ggg agg       1352
Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly Ala Gly Arg
420                 425                 430                 435


cgt gtt tgc ccc ggt gca caa ctt ggc atc aat ttg gtc aca tcc atg       1400
Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val Thr Ser Met
                440                 445                 450


atg ggt cac cta ttg cac cat ttc tat tgg agc cct cct aaa ggt gta       1448
Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro Lys Gly Val
                455                 460                 465


aaa cca gag gag att gac atg tca gag aat cca gga ttg gtc acc tac       1496
Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu Val Thr Tyr
                470                 475                 480


atg cga acc ccg gtg caa gct gtt ccc act cca agg ctg cct gct cac       1544
Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu Pro Ala His
                485                 490                 495


ttg tac aaa cgt gta gct gtg gat atg taattcttag tttgttatta             1591
Leu Tyr Lys Arg Val Ala Val Asp Met
500                 505
```

Fig. 4C

SEQ ID 1

```
ttcatgctct taaggttttg gactttgaac ttatgatgag atttgtaaaa ttccaagtga 1651

tcaaatgaag aaaagaccaa ataaaaaggc ttgacgattt aaaaaaaaaa aaaaaaa    1708
```

Fig. 4D

SEQ ID 2

Met Ala Phe Leu Leu Ile Pro Ile Ser Ile Ile Phe Ile Val Leu Ala
 1   5   10   15

Tyr Gln Leu Tyr Gln Arg Leu Arg Phe Lys Leu Pro Pro Gly Pro Arg
            20   25   30

Pro Trp Pro Ile Val Gly Asn Leu Tyr Asp Ile Lys Pro Val Arg Phe
        35   40   45

Arg Cys Phe Ala Glu Trp Ser Gln Ala Tyr Gly Pro Ile Ile Ser Val
        50   55   60

Trp Phe Gly Ser Thr Leu Asn Val Ile Val Ser Asn Ser Glu Leu Ala
 65   70   75   80

Lys Glu Val Leu Lys Glu Lys Asp Gln Gln Leu Ala Asp Arg His Arg
                85   90   95

Ser Arg Ser Ala Ala Lys Phe Ser Arg Asp Gly Gln Asp Leu Ile Trp
           100   105   110

Ala Asp Tyr Gly Pro His Tyr Val Lys Val Thr Lys Val Cys Thr Leu
        115   120   125

Glu Leu Phe Thr Pro Lys Arg Leu Glu Ala Leu Arg Pro Ile Arg Glu
        130   135   140

Asp Glu Val Thr Ala Met Val Glu Ser Ile Phe Asn Asp Thr Ala Asn
145   150   155   160

Pro Glu Asn Tyr Gly Lys Ser Met Leu Val Lys Lys Tyr Leu Gly Ala
                165   170   175

Val Ala Phe Asn Asn Ile Thr Arg Leu Ala Phe Gly Lys Arg Phe Val
                180   185   190

Asn Ser Glu Gly Val Met Asp Glu Gln Gly Leu Glu Phe Lys Glu Ile
            195   200   205

Val Ala Asn Gly Leu Lys Leu Gly Ala Ser Leu Ala Met Ala Glu His
        210   215   220

Ile Pro Trp Leu Arg Trp Met Phe Pro Leu Glu Glu Gly Ala Phe Ala
225   230   235   240

Fig. 4E

```
Lys His Gly Ala Arg Arg Asp Arg Leu Thr Arg Ala Ile Met Glu Glu
              245             250             255

His Thr Ile Ala Arg Lys Lys Ser Gly Gly Ala Gln Gln His Phe Val
              260             265             270

Asp Ala Leu Leu Thr Leu Gln Glu Lys Tyr Asp Leu Ser Glu Asp Thr
             275             280             285

Ile Ile Gly Leu Leu Trp Asp Met Ile Thr Ala Gly Met Asp Thr Thr
        290             295             300

Ala Ile Ser Val Glu Trp Ala Met Ala Glu Leu Ile Lys Asn Pro Arg
305             310             315             320

Val Gln Gln Lys Ala Gln Glu Glu Leu Asp Asn Val Leu Gly Ser Glu
              325             330             335

Arg Val Leu Thr Glu Leu Asp Phe Ser Ser Leu Pro Tyr Leu Gln Cys
             340             345             350

Val Ala Lys Glu Ala Leu Arg Leu His Pro Pro Thr Pro Leu Met Leu
         355             360             365

Pro His Arg Ala Asn Ala Asn Val Lys Ile Gly Gly Tyr Asp Ile Pro
    370             375             380

Lys Gly Ser Asn Val His Val Asn Val Trp Ala Val Ala Arg Asp Pro
385             390             395             400

Ala Val Trp Arg Asp Pro Leu Glu Phe Arg Pro Glu Arg Phe Ser Glu
             405             410             415

Asp Asp Val Asp Met Lys Gly His Asp Tyr Arg Leu Leu Pro Phe Gly
             420             425             430

Ala Gly Arg Arg Val Cys Pro Gly Ala Gln Leu Gly Ile Asn Leu Val
         435             440             445

Thr Ser Met Met Gly His Leu Leu His His Phe Tyr Trp Ser Pro Pro
    450             455             460

Lys Gly Val Lys Pro Glu Glu Ile Asp Met Ser Glu Asn Pro Gly Leu
465             470             475             480
```

Fig. 4F

SEQ ID 2

```
Val Thr Tyr Met Arg Thr Pro Val Gln Ala Val Pro Thr Pro Arg Leu
                485                 490                 495

Pro Ala His Leu Tyr Lys Arg Val Ala Val Asp Met
            500                 505
```

Fig. 4G

<400> 3

```
tgcaaacctg cacaaacaaa gagagagaag aagaaaaagg aagagaggag agagagagag  60


agagagagaa gcc atg gat tct tct ctt cat gaa gcc ttg caa cca cta      109
            Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu
             1               5                  10


ccc atg acg ctg ttc ttc att ata cct ttg cta ctc tta ttg ggc cta    157
Pro Met Thr Leu Phe Phe Ile Ile Pro Leu Leu Leu Leu Leu Gly Leu
         15                  20                  25


gta tct cgg ctt cgc cag aga cta cca tac cca cca ggc cca aaa ggc    205
Val Ser Arg Leu Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly
         30                  35                  40


tta ccg gtg atc gga aac atg ctc atg atg gat caa ctc act cac cga    253
Leu Pro Val Ile Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg
 45                  50                  55                  60


gga ctc gcc aaa ctc gcc aaa caa tac gc  ggt cta ttc cac ctc aag    301
Gly Leu Ala Lys Leu Ala Lys Gln Tyr G   Gly Leu Phe His Leu Lys
                 65                  70                  75


atg gga ttc tta cac atg gtg gcc gtt tcc aca ccc gac atg gct cgc    349
Met Gly Phe Leu His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg
                 80                  85                  90


caa gtc ctt caa gtc caa gac aac atc ttc tcg aac cgg cca gcc acc    397
Gln Val Leu Gln Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr
                 95                  100                 105


ata gcc atc agc tac ctc acc tat gac cga gcc gac atg gcc ttc gct    445
Ile Ala Ile Ser Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala
     110                 115                 120


cac tac ggc ccg ttt tgg cgt cag atg cgt aaa ctc tgc gtc atg aaa    493
His Tyr Gly Pro Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys
125                 130                 135                 140


tta ttt agc cgg aaa cga gcc gag tcg tgg gag tcg gtc cga gac gag    541
Leu Phe Ser Arg Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu
                 145                 150                 155


gtc gac tcg gca gta cga gtg gtc gcg tcc aat att ggg tcg acg gtg    589
Val Asp Ser Ala Val Arg Val Val Ala Ser Asn Ile Gly Ser Thr Val
                 160                 165                 170
```

Fig. 5A

SEQ ID 3

```
aat atc ggc gag ctg gtt ttt gct ctg acg aag aat att act tac agg    637
Asn Ile Gly Glu Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg
        175               180                185


gcg gct ttt ggg acg atc tcg cat gag gac cag gac gag ttc gtg gcc    685
Ala Ala Phe Gly Thr Ile Ser His Glu Asp Gln Asp Glu Phe Val Ala
        190               195                200


ata ctg caa gag ttt tcg cag ctg ttt ggt gct ttt aat ata gct gat    733
Ile Leu Gln Glu Phe Ser Gln Leu Phe Gly Ala Phe Asn Ile Ala Asp

205                   210               215               220


ttt atc cct tgg ctc aaa tgg gtt cct cag ggg att aac gtc agg ctc    781
Phe Ile Pro Trp Leu Lys Trp Val Pro Gln Gly Ile Asn Val Arg Leu
                225               230               235


aac aag gca cga ggg gcg ctt gat ggg ttt att gac aag atc atc gac    829
Asn Lys Ala Arg Gly Ala Leu Asp Gly Phe Ile Asp Lys Ile Ile Asp
            240               245               250


gat cat ata cag aag ggg agt aaa aac tcg gag gag gtt gat act gat    877
Asp His Ile Gln Lys Gly Ser Lys Asn Ser Glu Glu Val Asp Thr Asp
        255               260               265


atg gta gat gat tta ctt gct ttt tac ggt gag gaa gcc aaa gta agc    925
Met Val Asp Asp Leu Leu Ala Phe Tyr Gly Glu Glu Ala Lys Val Ser
        270               275               280


gaa tct gac gat ctt caa aat tcc atc aaa ctc acc aaa gac aac atc    973
Glu Ser Asp Asp Leu Gln Asn Ser Ile Lys Leu Thr Lys Asp Asn Ile
285               290               295               300


aaa gct atc atg gac gta atg ttt gga ggg acc gaa acg gtg gcg tcc   1021
Lys Ala Ile Met Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser
                305               310               315


gcg att gaa tgg gcc atg acg gag ctg atg aaa agc cca gaa gat cta   1069
Ala Ile Glu Trp Ala Met Thr Glu Leu Met Lys Ser Pro Glu Asp Leu
        320               325               330


aag aag gtc caa caa gaa ctc gcc gtg gtg gtg ggt ctt gac cgg cga   1117
Lys Lys Val Gln Gln Glu Leu Ala Val Val Val Gly Leu Asp Arg Arg
        335               340               345
```

Fig. 5B

```
gtc gaa gag aaa gac ttc gag aag ctc acc tac ttg ..a tgc gta ctg      1165
Val Glu Glu Lys Asp Phe Glu Lys Leu Thr Tyr Leu Lys Cys Val Leu
    350              355              360

aag gaa gtc ctt cgc ctc cac cca ccc atc cca ctc ctc ctc cac gag      1213
Lys Glu Val Leu Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu
365              370              375              380

act gcc gag gac gcc gag gtc ggc ggc tac tac att ccg gcg aaa tcg      1261
Thr Ala Glu Asp Ala Glu Val Gly Gly Tyr Tyr Ile Pro Ala Lys Ser
              385              390              395

cgg gtg atg atc aac gcg tgc gcc atc ggc cgg gac aag aac tcg tgg      1309
Arg Val Met Ile Asn Ala Cys Ala Ile Gly Arg Asp Lys Asn Ser Trp

        400              405              410

gcc gac cca gat acg ttt agg ccc tcc agg ttt ctc aaa gac ggt gtg      1357
Ala Asp Pro Asp Thr Phe Arg Pro Ser Arg Phe Leu Lys Asp Gly Val
        415              420              425

ccc gat ttc aaa ggg aac aac ttc gag ttc atc cca ttc ggg tca ggt      1405
Pro Asp Phe Lys Gly Asn Asn Phe Glu Phe Ile Pro Phe Gly Ser Gly
        430              435              440

cgt cgg tct tgc ccc ggt atg caa ctc gga ctc tac gcg cta gag acg      1453
Arg Arg Ser Cys Pro Gly Met Gln Leu Gly Leu Tyr Ala Leu Glu Thr
445              450              455              460

act gtg gct cac ctc ctt cac tgt ttc acg tgg gag ttg ccg gac ggg      1501
Thr Val Ala His Leu Leu His Cys Phe Thr Trp Glu Leu Pro Asp Gly
              465              470              475

atg aaa ccg agt gaa ctc gag atg aat gat gtg ttt gga ctc acc gcg      1549
Met Lys Pro Ser Glu Leu Glu Met Asn Asp Val Phe Gly Leu Thr Ala
              480              485              490

cca aga gcg att cga ctc acc gcc gtg ccg agt cca cgc ctt ctc tgt      1597
Pro Arg Ala Ile Arg Leu Thr Ala Val Pro Ser Pro Arg Leu Leu Cys
        495              500              505

cct ctc tat tgatcgaatg attggggggag ctttgtggag gggcttttat            1646
Pro Leu Tyr
        510
```

Fig. 5C

SEQ ID 3

```
ggagactcta tatatagatg ggaagtgaaa caacgacagg tgaatgcttg gatttttggt 1706

atatattggg gagggagggg aaaaaaaaaa taatgaaagg aaagaaaaga gagaatttga 1766

atttctcttc ctctgtggat aaaagcctcg tttttaattg tttttatgtg gagatatttg 1826

tgtttgttta tttttatctc ttttttttgca ataacactca aaataaaaa aaaaaaa    1883
```

Fig. 5D

SEQ ID 4

<400> 4

Met Asp Ser Ser Leu His Glu Ala Leu Gln Pro Leu Pro Met Thr Leu
 1   5   10   15

Phe Phe Ile Ile Pro Leu Leu Leu Leu Gly Leu Val Ser Arg Leu
             20   25   30

Arg Gln Arg Leu Pro Tyr Pro Pro Gly Pro Lys Gly Leu Pro Val Ile
         35   40   45

Gly Asn Met Leu Met Met Asp Gln Leu Thr His Arg Gly Leu Ala Lys
     50   55   60

Leu Ala Lys Gln Tyr Gly Gly Leu Phe His Leu Lys Met Gly Phe Leu
 65   70   75   80

His Met Val Ala Val Ser Thr Pro Asp Met Ala Arg Gln Val Leu Gln
             85   90   95

Val Gln Asp Asn Ile Phe Ser Asn Arg Pro Ala Thr Ile Ala Ile Ser
             100   105   110

Tyr Leu Thr Tyr Asp Arg Ala Asp Met Ala Phe Ala His Tyr Gly Pro
         115   120   125

Phe Trp Arg Gln Met Arg Lys Leu Cys Val Met Lys Leu Phe Ser Arg
     130   135   140

Lys Arg Ala Glu Ser Trp Glu Ser Val Arg Asp Glu Val Asp Ser Ala
145   150   155   160

Val Arg Val Val Ala Ser Asn Ile Gly Ser Thr Val Asn Ile Gly Glu
             165   170   175

Leu Val Phe Ala Leu Thr Lys Asn Ile Thr Tyr Arg Ala Ala Phe Gly
             180   185   190

Thr Ile Ser His Glu Asp Gln Asp Glu Phe Val Ala Ile Leu Gln Glu
         195   200   205

Phe Ser Gln Leu Phe Gly Ala Phe Asn Ile Ala Asp Phe Ile Pro Trp
     210   215   220

Leu Lys Trp Val Pro Gln Gly Ile Asn Val Arg Leu Asn Lys Ala Arg
225   230   235   240

Fig. 5E

Gly Ala Leu Asp Gly Phe Ile Asp Lys Ile Ile Asp Asp His Ile Gln
                    245   250   255

Lys Gly Ser Lys Asn Ser Glu Glu Val Asp Thr Asp Met Val Asp Asp
                260   265   270

Leu Leu Ala Phe Tyr Gly Glu Glu Ala Lys Val Ser Glu Ser Asp Asp
            275   280   285

Leu Gln Asn Ser Ile Lys Leu Thr Lys Asp Asn Ile Lys Ala Ile Met
        290   295   300

Asp Val Met Phe Gly Gly Thr Glu Thr Val Ala Ser Ala Ile Glu Trp
305   310   315   320

Ala Met Thr Glu Leu Met Lys Ser Pro Glu Asp Leu Lys Lys Val Gln
                325   330   335

Gln Glu Leu Ala Val Val Val Gly Leu Asp Arg Arg Val Glu Glu Lys
            340   345   350

Asp Phe Glu Lys Leu Thr Tyr Leu Lys Cys Val Leu Lys Glu Val Leu
            355   360   365

Arg Leu His Pro Pro Ile Pro Leu Leu Leu His Glu Thr Ala Glu Asp
        370   375   380

Ala Glu Val Gly Gly Tyr Tyr Ile Pro Ala Lys Ser Arg Val Met Ile
385   390   395   400

Asn Ala Cys Ala Ile Gly Arg Asp Lys Asn Ser Trp Ala Asp Pro Asp
                405   410   415

Thr Phe Arg Pro Ser Arg Phe Leu Lys Asp Gly Val Pro Asp Phe Lys
                420   425   430

Gly Asn Asn Phe Glu Phe Ile Pro Phe Gly Ser Gly Arg Arg Ser Cys
            435   440   445

Pro Gly Met Gln Leu Gly Leu Tyr Ala Leu Glu Thr Thr Val Ala His
        450   455   460

Leu Leu His Cys Phe Thr Trp Glu Leu Pro Asp Gly Met Lys Pro Ser
465   470   475   480

Fig. 5F

SEQ ID 4

```
Glu Leu Glu Met Asn Asp Val Phe Gly Leu Thr Ala Pro Arg Ala Ile
                485                 490                     495

Arg Leu Thr Ala Val Pro Ser Pro Arg Leu Leu Cys Pro Leu Tyr
            500                 505                 510
```

Fig. 5G

SEQ ID 10

<400> 10

```
aaacaccaat ttaatgggat ttcagatt :g tatcccatgc tattggctaa ggcatttttc 60

ttattgtaat ctaaccaatt ctaatttcca ccctggtgtg aactgactga caaatgcggt 120

ccgaaaacag cgaatgaaat gtctgggtga tcggtcaaac aagcggtggg cgagagagcg 180

cgggtgttgg cctagccggg atggggtag gtagacggcg tattaccggc gagttgtccg 240

aatggagttt tcggggtagg tagtaacgta gacgtcaatg gaaaaagtca taatctccgt 300

caaaaatcca accgctcctt cacatcgcag agttggtggc cacgggaccc tccacccact 360

cactcaatcg atcgcctgcc gtggttgccc attattcaac catacgccac ttgactcttc 420

accaacaatt ccaggccggc tttctataca atgtactgca caggaaaatc caatataaaa 480

agccggcctc tgcttccttc tcagtagccc ccagctcatt caattcttcc cactgcaggc 540

tacatttgtc agacacgttt tccgccattt ttcgcctgtt tctgcggaga atttgatcag 600

gttcggattg ggattgaatc aattgaaagg tttttatttt cagtatttcg atcgccatg 659
```

Fig. 6

<400> 11

```
ggccgggtgg tgacatttat tcataaattc atctcaaaac aagaaggatt tacaaaaata 60

aaagaaaaca aaattttcat ctttaacata attataattg tgttcacaaa attcaaactt 120

aaacccttaa tataaagaat ttctttcaac aatacacttt aatcacaact tcttcaatca 180

caacctcgtc caacaaaatt aaaatagatt aataaataaa taaacttaac tatttaaaaa 240

aaaatattat acaaaattta ttaaaacttc aaaataaaca aacttttat acaaaattca 300

tcaaaacttt aaaataaagc taaacactga aaatgtgagt acatttaaaa ggacgctgat 360

cacaaaaatt ttgaaaacat aaacaaactt gaaactctac cttttaagaa tgagtttgtc 420

gtctcattaa ctcattagtt ttatagttcg aatccaatta acgtatcttt tattttatgg 480

aataagggtg ttttaataag tgattttggg attttttag taatttattt gtgatatgtt 540

atggagtttt taaaaatata tatatatata tatattttg ggttgagttt acttaaaatt 600

tggaaaaggt tggtaagaac tataaattga gttgtgaatg agtgttttat ggattttta 660

agatgttaaa tttatatatg taattaaaat tttattttga ataacaaaaa ttataattgg 720

ataaaaaatt gttttgttaa atttagagta aaaattcaa aatctaaaat aattaaacac 780

tattatttt aaaaaatttg ttggtaaatt ttatcttata tttaagttaa aatttagaaa 840

aaattaattt taaattaata aacttttgaa gtcaaatatt ccaaatattt tccaaaatat 900

taaatctatt ttgcattcaa aatacaattt aaataataaa acttcatgga atagatta.i: 960

caatttgtat aaaaaccaaa aatctcaaat aaaatttaaa ttacaaaaca ttatcaacat 1020

tatgatttca agaaagacaa taaccagttt ccaataaaat aaaaaacctc atggcccgta 1080

attaagatct cattaattaa ttcttatttt ttaattttt tacatagaaa atatctttat 1140

attgtatcca agaaatatag aatgttctcg tccagggact attaatctcc aaacaagttt 1200

caaaatcatt acattaaagc tcatcatgtc atttgtggat tggaaattat attgtataag 1260

agaaatatag aatgttctcg tctagggact attaattcc aaacaaattt caaaat.jatt 1320
```

Fig. 7A

```
acattaaagc tcatcatgtc atttgtggat tggaaattag acaaaaaaaa tcccaaatat 1380

ttctctcaat ctcccaaaat atagttcgaa ctccatattt ttggaaattg agaatttttt 1440

tacccaataa tatatttttt tatacatttt agagattttc cagacatatt tgctctggga 1500

tttattggaa tgaaggttga gttataaact ttcagtaatc caagtatctt cggttttttga 1560

agatactaaa tccattatat aataaaaaca cattttaaac accaatttaa tgggatttca 1620

gatttgtatc ccatgctatt ggctaaggca tttttcttat tgtaatctaa ccaattctaa 1680

tttccaccct ggtgtgaact gactgacaaa tgcggtccga aaacagcgaa tgaaatgtct 1740

gggtgatcgg tcaacaagc ggtgggcgag agagcgcggg tgttggccta gccgggatgg 1800

gggtaggtag acggcgtatt accggcgagt tgtccgaatg gagttttcgg ggtaggtagt 1860

aacgtagacg tcaatggaaa aagtcataat ctccgtcaaa aatccaaccg ctccttcaca 1920

tcgcagagtt ggtggccacg ggaccctcca cccactcact cgatcgcctg ccgtggttgc 1980

ccattattca accatacgcc acttgactct tcaccaacaa ttccaggccg gctttctata 2040

caatgtactg cacaggaaaa tccaatataa aaagccggcc tctgcttcct tctcagtagc 2100

ccccagctca ttcaattctt cccactgcag gctacatttg tcagacacgt tttccgccat 2160

ttttcgcctg tttctgcgga gaatttgatc aggttcggat tgggattgaa tcaattgaaa 2220

ggttttttatt ttcagtattt cgatcgccat g                                2251
```

Fig. 7B

<400> 9

```
aaagataata tatgtgtatg cctactacta cacattgttt tgaagtgtgt aaacatagtg 60

caacactagg aggactcaca atgagcactt gttgacatga aactagctaa atgcccaaca 120

atat agtga aagctagtta aactaacccc tttgactttc aagatgatat atttatatcc 180

ctactacgtc ttcctctttt tgtctttctc ttgtgattaa accttccttg aaacaattct 240

caaatgtaaa attaaacctt gaaacttgta gagaccaaac ttccctagga gaaaccacat 300

ttatgacaac atatatacac caacccattg catactataa tattggaatt acctgcagcg 360

aacgaaagaa acgctgtctc accaactcgt gcactacatc ccgaaactta accttcccct 420

gatacagatt gaagagccga aaaaagcgtg catccaaatt tctggtatgg tgaggagccg 480

aaaaacgcgt gcgcctaatt tttttgagat gggccggaaa ataatgcgtg catctaaatt 540

ttcacgtgtc gcgtattggc gaggttgcgc tgaatgtgat cctgtgcgtg agccacattc 600

attccattgg ttgacccgcc ggtaccgcga ggaccgtggg gtctcacaga tacgcggatg 660

gtggatcagc actgagaaga ttagatgatg accaggcggg catttgaagt aaaaacttgg 720

gggtggttgg caagtacgcg acaaagaggg gtagtgcgca aggaagcgag ttggatgcaa 780

ataatattac aaagtgggtt ggtgggcatg agcatcaacc agaatgatgt tgttgctggt 840

tccgtgcaaa ttctgaccag tagtttgaac aatactaccc aacttgtttt tggtaaaaca 900

tgaagtgggt aaggagaatt gaacttacgt ctcatggtaa agggcaaggg caaatgactt 960

aacacatacc tttaactaat aaaaatacccc ctaacaaata cgaaaacgaa tgagttatca 1020

cagaccttca actaataaga tagccatcag acccacatct cctgactgac caaaaacaaa 1080

tgacttcaac caactaagat acccatcaaa gctaacccac aacccaattc ctcacttccc 1140

cttaccagac caaccaagca gacctacgcc attaactact ttaggacgtg ggaattgggg 1200

gtgccaccgt tgaagaatgg cactcaggt tggtaatccc tccacgtgta tgtagcagtc 1260

gtttggtgga dacggcgtgt ttgaatgtcc accttccagt ttggagaaca aggaaattgg 1320
```

Fig. 8A

SEQ ID 9

```
gcttatatta ggcctggatc tcttgtttca gagcaggagt agttcaggac aggaactagc 1380

attcaagaat tcaattgccc tgccctgctc tgctctgctt tgctcaactt attgatccct 1440

gctctggttt gttcaatttc ttgacccctg ctgggttctg ctctggtttg cacactttct 1500

cgattatata agtcattttg gatccttgca aggaagagaa tatg             1544
```

Fig. 8B
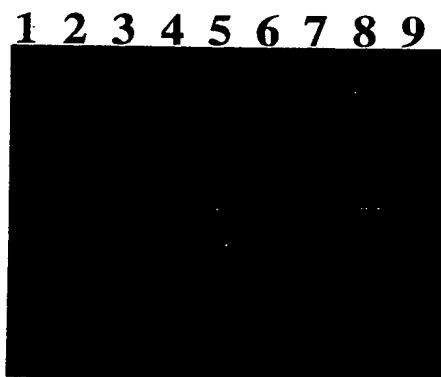
Lanes 1-4: PCR amplification of Sweetgum P450-1 gene from control and transgenic loblolly pine cell lines. Note the 600 bp amplified fragment in lanes 2-4.

Lanes 6-9: PCR amplification of Hygromycin gene from control and transgenic loblolly pine cell lines. Note the 1000 bp amplified fragment in lanes 7-9.

Lane 1: Control PT52 line
Lane 2: Transgenic line Y2
Lane 3: Transgenic line Y17
Lane 4: Control plasmid pSSLsP450-1-iml-s
Lane 5: DNA size marker Phi 174/HaeII (BRL); top 4 bands indicate molecular size of 1354, 1078, 872 and 603 bp.
Lane 6: Control PT52 line
Lane 7: Transgenic line Y7
Lane 8: Transgenic line O4
Lane 9: Control plasmid pHygro

FIG. 9